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Sequence Listing

<110> Biogen Idec Inc.
McLachlan, Karen
Gately, Dennis

<120> NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR TREATMENT AND
DIAGNOSIS OF COLON CARCINOMAS

<130> 037003-0302886

<140> PCT/US03/09534

<141> 2003-03-28

<150> US 60/367,727

<151> 2002-03-28

<150> US 60/381,328

<151> 2002-05-20

<150> US 60/386,747

<151> 2002-06-10

<150> US 60/427,564

<151> 2002-11-20

<160> 67

<170> PatentIn version 3.1

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His Ile Glu Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val
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Asn Glu Glu Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp
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Phe Ser Ser Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile
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Asp Thr Tyr Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala
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Val Cys Gln Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met
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Arg Asp Asp Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp
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Asn Glu Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro
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 180 185 190

Gly Ala Ala Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu
 195 200 205

Lys Arg Thr Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser
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Lys Gln Ala Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg
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Arg Glu Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp
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Leu Lys Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu
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Glu Asn Ile Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val
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Asn Met Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe
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Pro Val Leu Phe Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser
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Gly Gly Ala Ala Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro
65 70 75 80

Leu Lys Arg Thr Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro
85 90 95

Ser Lys Gln Ala Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val
100 105 110

Arg Arg Glu Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro
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Asp Leu Lys Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro
130 135 140

Glu Glu Asn Ile Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu
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Val Asn Met Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala
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Lys Glu Leu
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Glu Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser
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Pro Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala Tyr Leu
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Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly
 115 120 125

Lys Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val Met Val
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Val Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe Trp Lys
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His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val
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Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
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Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys
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Tyr Val Arg Arg Glu Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys
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U.S. Application No. - Unassigned
 Atty. Docket No. 037003-0312028

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His Leu Met Lys Phe Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr
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Pro Thr Pro Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu
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Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr
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Leu Pro Ser Tyr Arg Pro Gln Asp His Leu Gln Phe Pro Ala Leu Leu
565 570 575

Gly Met Leu Gly Pro Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro Phe
580 585 590

Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly Asp
595 600 605

Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val Phe
610 615 620

Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn Ala
625 630 635 640

Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu
645 650

<210> 12
<211> 186
<212> DNA
<213> Homo sapiens

<400> 12
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caaaaggctt tggtacataa aacattatfc cttccttggc ctaaaaactc atcgccacct 180
acatta 186

<210> 13
<211> 2333
<212> DNA
<213> Homo sapiens

<400> 13
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cctgtgacat tcttctggac aatgagtcct atcatctctc caccatgcac cttgtgactc 180
cctcctctgc tgacaacaga taaccacctt taactgtaac tttccacagc ctaccccgagc 240

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<210> 14
<211> 121
<212> PRT
<213> Homo sapiens

<400> 14

Met Gly Pro Val Pro His Ile Trp Gln Pro Asp Gln His Pro Gly Gln
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His Lys Asp Leu Gln Ser Glu Leu Leu Asn Phe Ser Ile Gln Thr Ala
20 25 30

Thr His Thr Tyr Gly Lys Arg Val Met Tyr His Arg Leu Ser Asn Arg
35 40 45

Glu Tyr Tyr Ser Tyr Asp Gly Lys Trp Gly Gln Lys Ala Leu Val His
50 55 60

Lys Thr Leu Phe Leu Pro Trp Pro Lys Asn Ser Ser Pro Pro Thr Leu
65 70 75 80

Lys Leu Ile Cys Leu Ile Thr Val Phe Arg Glu Leu Ile Leu Leu Gly
85 90 95

Gln Phe Gln Ala Gln Lys Tyr Ala Asn Trp His Leu Val Ser Tyr Ile
100 105 110

Lys Met His Pro Arg Pro Glu Thr Tyr
115 120

<210> 15
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 15

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<210> 16
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 16

Cys Cys Pro Ile Ala Ser Glu Ala Pro Trp Thr Ile Thr Asp Ala Glu
 1 5 10 15

Leu Arg Val Thr Leu Thr Val Glu Asp Ser Gln Pro Tyr Glu Asp Thr
 20 25 30

Leu Ala Gly Arg Ser Val Leu Val Lys Ser Leu Thr Pro Gln Thr Leu
 35 40 45

Gln Pro Gln Trp Thr Arg Pro Tyr Pro Val Ile Tyr Ser Thr Pro Thr
 50 55 60

Ala Val His Leu Gln Asp Pro Leu His Trp Val His His Ser Arg Ile
 65 70 75 80

Lys Pro Cys Pro Ser Asp Ser Gln Leu Asp Leu Ser Ser Ser Ser Trp
 85 90 95

Lys Pro Gln Asp
 100

<210> 17
 <211> 517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(517)
 <223> n is a, c, g, or t

<400> 17
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 gcactgtgaa cgccccagcc acaccgtgtc aacaaaccgt gtggcacttg ggagaaggca 180
 ggggtgattt acgantagtc atgtttcgcc tccacccgag tcaactgcaa ggagtggaca 240
 gtgacactga ataagcatnc ggngcacctc cttcggaag ggacttggt gacatggtag 300
 gccttccac tggagcctgt actttgtctt gctgggcagc actccantca tgggaaggaa 360

caatgancaa ggcgtggtgg tgggggtgng taggcctgag cgccgttttc catggtgacc 420
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<210> 18
 <211> 766
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(766)
 <223> n is a, c, g, or t

<400> 18
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 cgtttctgta catttcatgc agagcaatta aatagggcac tgcatttttc ttcaagttaa 180
 tttttattta ttaaagtaaa acataatgta ccttagaagc cagacagtcc tacaagctta 240
 ttatgttgta cagcggcggt ccgtccccct cccagccct ctctttctag aggcagccaa 300
 tttcagctgt ctctctctgc ttacctacat atttccatgt ttcttggttc atcacctggt 360
 ggcaccttca gtctggaaac acctgccctt cactttaggg gaattgggccc cctgttcggt 420
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 tcgaccattt tacttttctt gccatatttt caatgtttac tgatgtttct ctgccctttc 660
 agtgcacctt ggttttattt catgttagac tgaatccatg tgaaattgat aacagggttt 720
 cagccacac acacacacac aaaaaaaaaa aaaaaaaaaa aaaaaa 766

<210> 19
 <211> 455
 <212> DNA
 <213> Homo sapiens

<400> 19
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 agaaaggctt ttcaaacac acacgtgtgg acagaggctc acacacggat acgtgtgcac 180
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 gtgtacacac acaggcacag gcaccgtgtc ccaaggccat ctccaaggg caccgcaga 360
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455

<210> 20
<211> 1225
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1225)
<223> n is a, c, g, or t

<400> 20
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gttaagagat tcaacatttt ttccagaaat aacttctgaa aagggggcct nagattttga 180
acacttggga tcctaacagg ggggtgagaaa ggcttttcaa aacacacnac ggggtggacag 240
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gtgtccttcc tcgtgagagg atgatgaaga ggatgtggtt tccgccgcct catccacagg 540
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cgaggcattc tnaggggctn tatnc 1225

<210> 21
<211> 308
<212> DNA
<213> Homo sapiens

<400> 21
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cccactaact gagggaaaaa gggtccagg tggggctctc tgcccacttt gccaccacat	180
tcacattcca aatgggataa tgcctgaggg gccatgagtg gtcaggctgc cctgggggtga	240
atgtcaccct gatgaggccc atcagctctt gtccactcag tgaggccaga cttgtgctct	300
aatccact	308

<210> 22
 <211> 1212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1212)
 <223> n is a, c, g, or t

<400> 22	
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gtgctgatt caagcgtctg tctgggtcag atataaatac ccatgtgggt acctaggtgc	180
tagtctcccc actaactgag ggaaaaaggt tcccagggtg ggtcctctgc ccactttgcc	240
accacattca cattccaaat gggataatgc ctgaggggcc aagagtggtc aggtgcct	300
ggggtgaatg tcacctgat gagggccatc agctcttgct cactcagtga ggccagactt	360
gtgctctaata ccactctct gtgggtccct ggctgtatg gcttatactg gggagctggg	420
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catccttgct ctaagacaaa acttttccca gagaagaact ctttggtgt cccgctcagc	540
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cccnaggag ggagngana aggggtcatg ngttctgctn aanccnctgg ttggtataaa	960
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aaaaaaaaaa aa	1212

<210> 23
<211> 1229
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1229)
<223> n is a, c, g, or t

<400> 23
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ccgctgtacc tgtgcaatgc cagtgatgac gacaatctgg agcctggatt catcagcatc 180
gtcaagctgg agagtccctg acggggcccc cgcccctgcc tgtcactggc tagcaaggct 240
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acnccccna ttccctntnn anganccctn ngtttncnccn agggccctna cccgggcenn 1200
gccccnaaa caaagggant tganaaant 1229

<210> 24
<211> 3780
<212> DNA
<213> Homo sapiens

<400> 24
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aagcataaat gttcttttcc tccatttgtc tggatctgag aacctgcatt tggatttagc 120

tagtgggaagc agtatgtatg gttgaagtgc attgctgcag ctggtagcat gagtgggtggc	180
caccagctgc agctggctgc cctctggccc tggtctgtga tggtaccct gcaggcaggc	240
tttggacgca caggactggt actggcagca gcggtggagt ctgaaagatc agcagaacag	300
aaagctgtta tcagagtgat ccccttgaaa atggacccca caggaaaact gaatctcact	360
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tccccccac tgtacctgtg caatgccagt gatgacgaca atctggagcc tggattcatc	480
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Lys Leu Met Gln Ser His Pro Leu Tyr Leu Cys Asn Ala Ser Asp Asp
85 90 95

Asp Asn Leu Glu Pro Gly Phe Ile Ser Ile Val Lys Leu Glu Ser Pro
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Arg Arg Ala Pro Arg Pro Cys Leu Ser Leu Ala Ser Lys Ala Arg Met
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Val Val Leu Ile Trp Gly Asn Asp Ala Glu Lys Leu Met Glu Phe Val
165 170 175

Tyr Lys Asn Gln Lys Ala His Val Arg Ile Glu Leu Lys Glu Pro Pro
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Ala Trp Pro Asp Tyr Asp Val Trp Ile Leu Met Thr Val Val Gly Thr
195 200 205

Ile Phe Val Ile Ile Leu Ala Ser Val Leu Arg Ile Arg Cys Arg Pro
210 215 220

Arg His Ser Arg Pro Asp Pro Leu Gln Gln Arg Thr Ala Trp Ala Ile
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Ala Ile Cys Leu Glu Glu Phe Ser Glu Gly Gln Glu Leu Arg Val Ile
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Ser Cys Leu His Glu Phe His Arg Asn Cys Val Asp Pro Trp Leu His
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Gln His Arg Thr Cys Pro Leu Cys Val Phe Asn Ile Thr Glu Gly Asp
 305 310 315 320

Ser Phe Ser Gln Ser Leu Gly Pro Ser Arg Ser Tyr Gln Glu Pro Gly
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Arg Arg Leu His Leu Ile Arg Gln His Pro Gly His Ala His Tyr His
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 355 360 365

Pro Pro Arg Pro Gly Pro Phe Leu Pro Ser Gln Glu Pro Gly Met Gly
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Pro Arg His His Arg Phe Pro Arg Ala Ala His Pro Arg Ala Pro Gly
 385 390 395 400

Glu Gln Gln Arg Leu Ala Gly Ala Gln His Pro Tyr Ala Gln Gly Trp
 405 410 415

Gly Met Ser His Leu Gln Ser Thr Ser Gln His Pro Ala Ala Cys Pro
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Val Pro Leu Arg Arg Ala Arg Pro Pro Asp Ser Ser Gly Ser Gly Glu
 435 440 445

Ser Tyr Cys Thr Glu Arg Ser Gly Tyr Leu Ala Asp Gly Pro Ala Ser
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 465 470 475 480

Asn Cys Thr Asp Ile Ser Leu Gln Gly Val His Gly Ser Ser Ser Thr
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Arg Pro Arg Ser Leu Asp Ser Val Val Pro Thr Gly Glu Thr Gln Val
530 535 540

Ser Ser His Val His Tyr His Arg His Arg His His His Tyr Lys Lys
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Arg Phe Gln Trp His Gly Arg Lys Pro Gly Pro Glu Thr Gly Val Pro
565 570 575

Gln Ser Arg Pro Pro Ile Pro Arg Thr Gln Pro Gln Pro Glu Pro Pro
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Ser Pro Asp Gln Gln Val Thr Gly Ser Asn Ser Ala Ala Pro Ser Gly
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Arg Leu Ser Asn Pro Gln Cys Pro Arg Ala Leu Pro Glu Pro Ala Pro
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Gly Pro Val Asp Ala Ser Ser Ile Cys Pro Ser Thr Ser Ser Leu Phe
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Asn Leu Gln Lys Ser Ser Leu Ser Ala Arg His Pro Gln Arg Lys Arg
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660 665 670

Thr Val His Pro Ala Cys Gln Ile Phe Pro His Tyr Thr Pro Ser Val
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Ala Tyr Pro Trp Ser Pro Glu Ala His Pro Leu Ile Cys Gly Pro Pro
690 695 700

Gly Leu Asp Lys Arg Leu Leu Pro Glu Thr Pro Gly Pro Cys Tyr Ser
705 710 715 720

Asn Ser Gln Pro Val Trp Leu Cys Leu Thr Pro Arg Gln Pro Leu Glu
725 730 735

Pro His Pro Pro Gly Glu Gly Pro Ser Glu Trp Ser Ser Asp Thr Ala
740 745 750

Glu Gly Arg Pro Cys Pro Tyr Pro His Cys Gln Val Leu Ser Ala Gln
755 760 765

Pro Gly Ser Glu Glu Glu Leu Glu Glu Leu Cys Glu Gln Ala Val
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 <213> Homo sapiens

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 <223> n is a, c, g, or t

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 <212> DNA
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(1119)
 <223> n is a, c, g, or t

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1058)

<223> n is a, c, g, or t

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<213> Homo sapiens

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<400> 32

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35 40 45

Ala Val Asp Trp Leu Tyr Asp Leu Leu Arg Asn Asn Ser Asn Phe Gly
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Pro Glu Val Thr Arg Gln Gln Thr Ile Gln Leu Leu Arg Lys Phe Leu
65 70 75 80

Lys Asn His Val Ile Glu Asp Ile Lys Gly Arg Trp Gly Ser Glu Asn
85 90 95

Val Asp Asp Asn Asn Gln Leu Phe Arg Phe Pro Ala Thr Ser Pro Leu
100 105 110

Lys Thr Leu Pro Arg Arg Tyr Pro Glu Leu Arg Lys Asn Asn Ile Glu
115 120 125

Asn Phe Ser Lys Asp Lys Asp Ser Ile Phe Lys Leu Arg Asn Leu Ser
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Asp Asn Arg Glu Leu Ser Gln Glu Asp Val Glu Glu Val Trp Arg Tyr
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Val Ile Leu Ile Tyr Leu Gln Thr Ile Leu Gly Val Pro Ser Leu Glu
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Val Cys Gly Tyr Ile Thr Val Ser Asp Arg Ser Ser Gly Ile His Lys
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<400> 38

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<400> 40

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Val Ala Pro Pro Leu Pro Ala Ala Asp Ala Ala His Glu Phe Thr Val
35 40 45

Tyr Arg Met Gln Gln Tyr Asp Leu Gln Gly Gln Pro Tyr Gly Thr Arg
50 55 60

Asn Ala Val Leu Asn Thr Glu Ala Arg Thr Met Ala Ala Glu Val Leu
65 70 75 80

Ser Arg Arg Cys Val Leu Met Arg Leu Leu Asp Phe Ser Tyr Glu Gln
85 90 95

Tyr Gln Lys Ala Leu Arg Gln Ser Ala Gly Ala Val Val Ile Ile Leu
100 105 110

Pro Arg Ala Met Ala Ala Val Pro Gln Asp Val Val Arg Gln Phe Met
115 120 125

Glu Ile Glu Pro Glu Met Leu Ala Met Glu Thr Ala Val Pro Val Tyr
130 135 140

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Phe Ala Val Glu Asp Glu Ala Leu Leu Ser Ile Tyr Lys Gln Thr Gln
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Ala Ala Ser Ala Ser Gln Gly Ser Ala Ser Ala Ala Glu Val Leu Leu
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Ser Lys Ala Val Ser Asp Trp Leu Ile Ala Ser Val Glu Gly Arg Leu
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Thr Gly Leu Gly Gly Glu Asp Leu Pro Thr Ile Val Ile Val Ala His
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Tyr Asp Ala Phe Gly Val Ala Pro Trp Leu Ser Leu Gly Ala Asp Ser
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325 330 335

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Gly Thr Pro Pro Asp Met Pro Val Phe Thr Glu Gln Met Gln Ile Gln
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Gln Glu Gln Leu Asp Ser Val Met Asp Trp Leu Thr Asn Gln Pro Arg
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Ala Ala Gln Leu Val Asp Lys Asp Ser Thr Phe Leu Ser Thr Leu Glu
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Val Met Asn Ala Tyr Arg Val Lys Pro Ala Val Phe Asp Leu Leu Leu
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 35 40 45

Ile Ile Ile Trp Val Leu Val Met Tyr Ile Gly Gln Val Ala Lys Asp
 50 55 60

Val Leu Lys Trp Pro Arg Pro Ser Ser Pro Pro Val Val Lys Leu Glu
 65 70 75 80

Lys Arg Leu Ile Ala Glu Tyr Gly Met Pro Ser Thr His Ala Met Ala
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Ala Thr Ala Ile Ala Phe Thr Leu Leu Ile Ser Thr Met Asp Arg Tyr
 100 105 110

Gln Tyr Pro Phe Val Leu Gly Leu Val Met Ala Val Val Phe Ser Thr
 115 120 125

Leu Val Cys Leu Ser Arg Leu Tyr Thr Gly Met His Thr Val Leu Asp
 130 135 140

Val Leu Gly Gly Val Leu Ile Thr Ala Leu Leu Ile Val Leu Thr Tyr
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Pro Ala Trp Thr Phe Ile Asp Cys Leu Asp Ser Ala Ser Pro Leu Phe
 165 170 175

Pro Val Cys Val Ile Val Val Pro Phe Phe Leu Cys Tyr Asn Tyr Pro
 180 185 190

Val Ser Asp Tyr Tyr Ser Pro Thr Arg Ala Asp Thr Thr Thr Ile Leu
 195 200 205

Ala Ala Gly Ala Gly Val Thr Ile Gly Phe Trp Ile Asn His Phe Phe
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Gln Leu Val Ser Lys Pro Ala Glu Ser Leu Pro Val Ile Gln Asn Ile
 225 230 235 240

Pro Pro Leu Thr Thr Tyr Met Leu Val Leu Gly Leu Thr Lys Phe Ala
 245 250 255

Val Gly Ile Val Leu Ile Leu Leu Val Arg Gln Leu Val Gln Asn Leu
 260 265 270

Ser Leu Gln Val Leu Tyr Ser Trp Phe Lys Val Val Thr Arg Asn Lys
 275 280 285

Glu Ala Arg Arg Arg Leu Glu Ile Glu Val Pro Tyr Lys Phe Val Thr
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Tyr Thr Ser Val Gly Ile Cys Ala Thr Thr Phe Val Pro Met Leu His
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Arg Phe Leu Gly Leu Pro
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35 40 45

Leu Asp Val Leu Gly Gly Val Leu Ile Thr Ala Leu Leu Ile Val Leu
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Thr Tyr Pro Ala Trp Thr Phe Ile Asp Cys Leu Asp Ser Ala Ser Pro
65 70 75 80

Leu Phe Pro Val Cys Val Ile Val Val Pro Phe Phe Leu Cys Tyr Asn
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Tyr Pro Val Ser Asp Tyr Tyr Ser Pro Thr Arg Ala Asp Thr Thr Thr
100 105 110

Ile Leu Ala Ala Gly Ala Gly Val Thr Ile Gly Phe Trp Ile Asn His
115 120 125

Phe Phe Gln Leu Val Ser Lys Pro Ala Glu Ser Leu Pro Val Ile Gln
130 135 140

Asn Ile Pro Pro Leu Thr Thr Tyr Met Leu Val Leu Gly Leu Thr Lys
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Phe Ala Val Gly Ile Val Leu Ile Leu Leu Val Arg Gln Leu Val Gln
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Asn Leu Ser Leu Gln Val Leu Tyr Ser Trp Phe Lys Val Val Thr Arg
180 185 190

Asn Lys Glu Ala Arg Arg Arg Leu Glu Ile Glu Val Pro Tyr Lys Phe
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Leu His Arg Phe Leu Gly Leu Pro
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<213> Homo sapiens

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<211> 552
<212> PRT
<213> Homo sapiens

<400> 50

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35 40 45

Pro Tyr Gly Thr Arg Asn Ala Val Leu Asn Thr Glu Ala Arg Thr Met
50 55 60

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Ala Ala Glu Val Leu Ser Arg Arg Cys Val Leu Met Arg Leu Leu Asp
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Phe Ser Tyr Glu Gln Tyr Gln Lys Ala Leu Arg Gln Ser Ala Gly Ala
85 90 95

Val Val Ile Ile Leu Pro Arg Ala Met Ala Ala Val Pro Gln Asp Val
100 105 110

Val Arg Gln Phe Met Glu Ile Glu Pro Glu Met Leu Ala Met Glu Thr
115 120 125

Ala Val Pro Val Tyr Phe Ala Val Glu Asp Glu Ala Leu Leu Ser Ile
130 135 140

Tyr Lys Gln Thr Gln Ala Ala Ser Ala Ser Gln Gly Ser Ala Ser Ala
145 150 155 160

Ala Glu Val Leu Leu Arg Thr Ala Thr Ala Asn Gly Phe Gln Met Val
165 170 175

Thr Ser Gly Val Gln Ser Lys Ala Val Ser Asp Trp Leu Ile Ala Ser
180 185 190

Val Glu Gly Arg Leu Thr Gly Leu Gly Gly Glu Asp Leu Pro Thr Ile
195 200 205

Val Ile Val Ala His Tyr Asp Ala Phe Gly Val Ala Pro Trp Leu Ser
210 215 220

Leu Gly Ala Asp Ser Asn Gly Ser Gly Val Ser Val Leu Leu Glu Leu
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Ala Arg Leu Phe Ser Arg Leu Tyr Thr Tyr Lys Arg Thr His Ala Ala
245 250 255

Tyr Asn Leu Leu Phe Phe Ala Ser Gly Gly Gly Lys Phe Asn Tyr Gln
260 265 270

Gly Thr Lys Arg Trp Leu Glu Asp Asn Leu Asp His Thr Asp Ser Ser
275 280 285

Leu Leu Gln Asp Asn Val Ala Phe Val Leu Cys Leu Asp Thr Val Gly
290 295 300

Arg Gly Ser Ser Leu His Leu His Val Ser Lys Pro Pro Arg Glu Gly
305 310 315 320

Thr Leu Gln His Ala Phe Leu Arg Glu Leu Glu Thr Val Ala Ala His
325 330 335

Gln Phe Pro Glu Val Arg Phe Ser Met Val His Lys Arg Ile Asn Leu
340 345 350

Ala Glu Asp Val Leu Ala Trp Glu His Glu Arg Phe Ala Ile Arg Arg
355 360 365

Leu Pro Ala Phe Thr Leu Ser His Leu Glu Ser His Arg Asp Gly Gln
370 375 380

Arg Ser Ser Ile Met Asp Val Arg Ser Arg Val Asp Ser Lys Thr Leu
385 390 395 400

Thr Arg Asn Thr Arg Ile Ile Ala Glu Ala Leu Thr Arg Val Ile Tyr
405 410 415

Asn Leu Thr Glu Lys Gly Thr Pro Pro Asp Met Pro Val Phe Thr Glu
420 425 430

Gln Met Gln Ile Gln Gln Glu Gln Leu Asp Ser Val Met Asp Trp Leu
435 440 445

Thr Asn Gln Pro Arg Ala Ala Gln Leu Val Asp Lys Asp Ser Thr Phe
450 455 460

Leu Ser Thr Leu Glu His His Leu Ser Arg Tyr Leu Lys Asp Val Lys
465 470 475 480

Gln His His Val Lys Ala Asp Lys Arg Asp Pro Glu Phe Val Phe Tyr
485 490 495

Asp Gln Leu Lys Gln Val Met Asn Ala Tyr Arg Val Lys Pro Ala Val
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Phe Asp Leu Leu Leu Ala Val Gly Ile Ala Ala Tyr Leu Gly Met Ala
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<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 53

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 35 40 45

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Tyr Asn Glu Glu Phe Thr Trp Arg Leu Gly Glu Asn Tyr Ala Glu Glu
 85 90 95

Tyr Ala Lys Ala Leu Glu Lys Gly Leu Pro Asp Pro Val Leu Tyr Leu
 100 105 110

Ala Glu Lys Phe Thr Pro Arg Ser Pro Cys Gly Leu Tyr Arg Gln Tyr
 115 120 125

Arg Leu Ala Gly His Tyr Thr Ser Ala Met Leu Trp Val Ala Phe Leu
 130 135 140

Cys Trp Leu Leu Ala Asn Val Met Leu Ser Met Pro Val Leu Val Tyr
 145 150 155 160

Gly Gly Tyr Met Leu Leu Ala Thr Gly Ile Phe Gln Leu Leu Ala Leu
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Leu Phe Phe Ser Met Ala Thr Ser Leu Thr Ser Pro Cys Pro Leu His
 180 185 190

Leu Gly Ala Ser Val Leu His Thr His His Gly Pro Ala Phe Trp Ile
 195 200 205

Thr Leu Thr Thr Gly Leu Leu Cys Val Leu Leu Gly Leu Ala Met Ala
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Val Ala His Arg Met Gln Pro His Arg Leu Lys Ala Phe Phe Asn Gln
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Ser Val Asp Glu Asp Pro Met Leu Glu Trp Ser Pro Glu Glu Gly Gly
 245 250 255

Leu Leu Ser Pro Arg Tyr Arg Ser Met Ala Asp Ser Pro Lys Ser Gln
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<400> 55

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Ala Leu Ala Ala Ser Phe Leu Leu Ile Leu Pro Gly Ile Arg Gly His
35 40 45

Ser Arg Trp Phe Trp Leu Val Arg Val Leu Leu Ser Leu Phe Ile Gly
50 55 60

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100 105 110

Thr Gly Thr Pro Val His Gln Leu Asn Glu Thr Ile Asp Tyr Asn Glu
115 120 125

Gln Phe Thr Trp Arg Leu Lys Glu Asn Tyr Ala Ala Glu Tyr Ala Asn
130 135 140

Ala Leu Glu Lys Gly Leu Pro Asp Pro Val Leu Tyr Leu Ala Glu Lys
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Phe Thr Pro Ser Ser Pro Cys Gly Leu Tyr His Gln Tyr His Leu Ala
165 170 175

Gly His Tyr Ala Ser Ala Thr Leu Trp Val Ala Phe Cys Phe Trp Leu
180 185 190

Leu Ser Asn Val Leu Leu Ser Thr Pro Ala Pro Leu Tyr Gly Gly Leu
195 200 205

Ala Leu Leu Thr Thr Gly Ala Phe Ala Leu Phe Gly Val Phe Ala Leu
210 215 220

Ala Ser Ile Ser Ser Val Pro Leu Cys Pro Leu Arg Leu Gly Ser Ser
225 230 235 240

Ala Leu Thr Thr Gln Tyr Gly Ala Ala Phe Trp Val Thr Leu Ala Thr
245 250 255

Gly Glu Asp Arg Glu Asn Gly Pro Arg Gly Leu Arg Val Glu Thr Gly
260 265 270

Phe Thr Pro Gly Val Leu Cys Leu Phe Leu Gly Gly Ala Val Ala Gly
275 280 285

Lys Gln Cys Pro Pro Gly Leu Gly Gln Glu Ser Ser Arg Lys Gly Thr
290 295 300

Glu Arg Cys Trp Arg Glu Ala Ser Asp Ile Arg Arg His Gln Gly Lys
305 310 315 320

Ser Pro Gly Ala Ile Cys Lys
 325

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 <211> 405
 <212> DNA
 <213> Homo sapiens

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Leu Pro Cys Pro Ser Pro Pro Thr Leu His Gly Asp Glu His Leu Ser
 35 40 45

Trp Phe Cys Ser Pro Ala Ala Gly Ser Phe Thr Thr Leu Val Ala Gln
 50 55 60

Val Gln Val Gly Arg Pro Ala Pro Asp Pro Gly Lys Pro Gly Arg Glu
 65 70 75 80

Ser Arg Leu Arg Leu Leu Gly Asn Tyr Ser Leu Trp Leu Glu Gly Ser
 85 90 95

Lys Glu Glu Asp Ala Gly Arg Tyr Trp Cys Ala Val Leu Gly Gln His
 100 105 110

His Asn Tyr Gln Asn Trp Arg Val Tyr Asp Val Leu Val Leu Lys Gly
 115 120 125

Ser Gln Leu Ser Ala Arg Ala Ala Asp Gly Ser Pro Cys Asn Val Leu
 130 135 140

Leu Cys Ser Val Val Pro Ser Arg Arg Met Asp Ser Val Thr Trp Gln
 145 150 155 160

Glu Gly Lys Gly Pro Val Arg Gly Arg Val Gln Ser Phe Trp Gly Ser
 165 170 175

Glu Ala Ala Leu Leu Leu Val Cys Pro Gly Glu Gly Leu Ser Glu Pro
180 185 190

Arg Ser Arg Arg Pro Arg Ile Ile Arg Cys Leu Met Thr His Asn Lys
195 200 205

Gly Val Ser Phe Ser Leu Ala Ala Ser Ile Asp Ala Ser Pro Ala Leu
210 215 220

Cys Ala Pro Ser Thr Gly Trp Asp Met Pro Trp Ile Leu Met Leu Leu
225 230 235 240

Leu Thr Met Gly Gln Gly Val Val Ile Leu Ala Leu Ser Ile Val Leu
245 250 255

Trp Arg Gln Arg Val Arg Gly Ala Pro Gly Arg Gly Asn Arg Met Arg
260 265 270

Cys Tyr Asn Cys Gly Gly Ser Pro Ser Ser Ser Cys Lys Glu Ala Val
275 280 285

Thr Thr Cys Gly Glu Gly Arg Pro Gln Pro Gly Leu Glu Gln Ile Lys
290 295 300

Leu Pro Gly Asn Pro Pro Val Thr Leu Ile His Gln His Pro Ala Cys
305 310 315 320

Val Ala Ala His His Cys Asn Gln Val Glu Thr Glu Ser Val Gly Asp
325 330 335

Val Thr Tyr Pro Ala His Arg Asp Cys Tyr Leu Gly Asp Leu Cys Asn
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Ser Ala Val Ala Ser His Val Ala Pro Ala Gly Ile Leu Ala Ala Ala
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6

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21